



#6

## SEQUENCE LISTING

&lt;110&gt; Scott, Fred W.

&lt;120&gt; Recombinant Multivalent Viral Vaccine

&lt;130&gt; 18617.0016

&lt;140&gt; US 09/873,881

&lt;141&gt; 2001-06-04

&lt;150&gt; US 08/552,369

&lt;151&gt; 1995-11-03

&lt;160&gt; 19

&lt;210&gt; 1

&lt;211&gt; 2254

&lt;212&gt; DNA

&lt;213&gt; feline panleukopenia virus

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 1

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Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile	

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Phe	Asn	Pro	Gly	Asp	Trp	Gln	Leu	Ile	Val	Asn	Thr	Met	Ser	Glu						
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Thr	Asn	Phe	Gly	Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly		
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				335					340					345		
gaa	gcg	tct	aca	caa	ggg	cca	ttt	aaa	ata	cct	att	gca	gca	gga	1080	
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cca	aga	tat	gca	ttt	ggt	aga	caa	cat	ggt	caa	aaa	act	act	aca	1170	
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Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp		
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Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro		
				455					460					465		
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Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro	
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ggt caa tta ttt gta aaa gtt gcg cct aat tta aca aat gaa tat	1530
Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr	
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gat cct gat gca tct gct aat atg tca aga att gta act tac tca	1575
Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser	
515 520 525	
gat ttt tgg tgg aaa ggt aaa tta gta ttt aaa gct aaa cta aga	1620
Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg	
530 535 540	
gca tct cat act tgg aat cca att caa caa atg agt att aat gta	1665
Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val	
545 550 555	
gat aac caa ttt aac tat cta cca aat aat att gga gct atg aaa	1710
Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys	
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Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr	
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<220>

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cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac	84
Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp	
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aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc	126
Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser	
30 35 40	
tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac	168
Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn	
45 50 55	
ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc	210
Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile	
60 65 70	
tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg	252
Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val	
75 80	
acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca	294
Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr	
85 90 95	
acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca	336
Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala	
100 105 110	
tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga	378
Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg	
115 120 125	
tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg	420
Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp	
130 135 140	
ctt cga act gta aaa acc acc aag gag tct ctc gtt atc ata	462

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Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu	
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cac	tcg	agg	gtc	ttc	cct	agc	ggg	aag	tgc	tca	gga	gta	gcg	546
His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala	
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gtg	tct	tct	acc	tac	tgc	tcc	act	aac	cac	gat	tac	acc	att	588
Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile	
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tgg	atg	ccc	gag	aat	ccg	aga	cta	ggg	atg	tct	tgt	gac	att	630
Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile	
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Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu	
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aaa	gga	gca	tgc	aaa	ctc	aag	tta	tgt	gga	gtt	cta	gga	ctt	756
Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu	
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aga	ctt	atg	gat	gga	aca	tgg	gtc	gcg	atg	caa	aca	tca	aat	798
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gac	ttt	cgc	tca	gac	gaa	att	gag	cac	ctt	gtt	gta	gag	gag	882
Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu	
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Leu	Val	Arg	Lys	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser	
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Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His	
	310					315					320			

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Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile	
325 330 335	
ttc aac aag acc ttg atg gaa gcc gat gct cac tac aag tca	1050
Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser	
340 345 350	
gtc aga act tgg aat gag atc ctc cct tca aaa ggg tgt tta	1092
Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu	
355 360	
aga gtt ggg ggg agg tgt cat cct cat gtg aac ggg gtg ttt	1134
Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe	
365 370 375	
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc	1176
Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile	
380 385 390	
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg	1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu	
395 400 405	
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Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp	
410 415 420	
ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt	1302
Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe	
425 430	
gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga	1344
Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly	
435 440 445	
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg	1386
Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu	
450 455 460	
agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg	1428
Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu	
465 470 475	
atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa	1470
Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln	
480 485 490	
cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc	1512
His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro	

495

500

caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt 1554  
Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser  
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ggg ggt gag acc aga ctg tga 1575  
Gly Gly Glu Thr Arg Leu  
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<213> P11 late promoter and leader sequence

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<213> artificial sequence

<220>  
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<213> artificial sequence

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<223> sequencing primer

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ctacttgcat agataggt 18

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cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt	90
Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val	
20 25 30	
ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta	135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu	
35 40 45	
cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa	180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln	
50 55 60	
gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act	225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr	
65 70 75	
cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa	270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu	
80 85 90	
gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac	315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His	
95 100 105	
ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt	360
Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu	
110 115 120	
ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag	405

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Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu		
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Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr		
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tct	gaa	act	cag	ggg	aag	ata	ctc	ttt	aaa	caa	tcc	tta	gga	cca	585	
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro		
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Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala		
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tgg	tct	ggt	tct	gtt	gat	gtt	agg	ttt	tct	att	tct	gga	tct	ggt	675	
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly		
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gtc	ttt	gga	ggg	aaa	tta	gct	gct	att	gtt	gtg	ccg	cca	gga	att	720	
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile		
				230					235					240		
gat	cct	gtt	caa	agt	act	tca	atg	ctg	caa	tat	cct	cat	gtc	ctc	765	
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu		
				245					250					255		
ttt	gat	gct	cgt	caa	gtt	gaa	cct	gtt	atc	ttt	tcc	att	ccc	gat	810	
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp		
				260					265					270		
cta	aga	agc	acc	tta	tat	cac	ctt	atg	tct	gac	act	gat	acc	aca	855	
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr		
				275					280					285		
tcg	ttg	gta	atc	atg	gtg	tac	aat	gat	ctt	att	aac	ccc	tat	gct	900	
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala		
				290					295					300		
aat	gac	tca	aac	tct	tcg	ggc	tgc	att	gtc	act	gtg	gaa	act	aaa	945	
Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys		
				305					310					315		

ccg ggg cca gat ttc aag ttt cac ctc tta aaa cct cct ggg tct	990
Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser	
320 325 330	
atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035
Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser	
335 340 345	
tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp	
350 355 360	
ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125
Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp	
365 370 375	
ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca	1170
Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro	
380 385 390	
att act atc act atc agt gtt aag gag tca gca aag ctt ggt att	1215
Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile	
395 400 405	
gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg	1260
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp	
410 415 420	
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat	1305
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr	
425 430 435	
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag	1350
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln	
440 445 450	
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc	1395
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly	
455 460 465	
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag	1440
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys	
470 475 480	
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc	1485
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	
485 490 495	
aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val	
500 505 510	

ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac	1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp	
515 520 525	
aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att	1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile	
530 535 540	
ggt gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa	1665
Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu	
545 550 555	
cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct	1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser	
560 565 570	
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser	
575 580 585	
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta	1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu	
590 595 600	
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn	
605 610 615	
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe	
620 625 630	
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc	1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala	
635 640 645	
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn	
650 655 660	
att agg agt gtg atg aca aaa tta tga	2007
Ile Arg Ser Val Met Thr Lys Leu	
665	

<210> 8

<211> 582

<212> DNA

<213> artificial sequence

<220>

<223> hemagglutinin left arm

<400> 8

attaaacgca	aatatccatg	gaaaacgcgc	agtatacaga	cgattttttta	50
cagtatttgg	agagttttat	aggaagtata	tagagtagaa	ccagaatttt	100
gtaaaaataa	atcacatttt	tatactaata	tgaaacaact	atcgatagtt	150
atattgctac	tatcgatagt	atatacaacc	aaacctcatc	ctacacagat	200
atcaaaaaaa	ctaggcgatg	atgctactct	atcgtgtaat	agaaacaata	250
cacatggata	tcttgtcatg	agttcttggg	ataagaaacc	agactccatt	300
attctcttag	cagccaaaaa	cgatgtcgta	tactttgatg	attatacagc	350
ggataaagta	tcatacgatt	caccgtatga	tactctagct	acaattatta	400
caattaaatc	attgacatct	gcagatgcag	gtacttatat	atgcgcattc	450
tttataacat	caacaaatga	tacggataaa	atagattatg	aagaatactt	500
catagatttg	gttgtaaadc	cagctaattg	atccactatt	gacgcgattc	550
tatcaggatc	taatttctcc	gtgataggta	tc		582

<210> 9

<211> 447

<212> DNA

<213> artificial sequence

<220>

<223> hemagglutinin right arm

<400> 9

ctctagcgcc	taaccccagg	cgaccgacga	caacctttat	gatacatata	50
atgaaccaat	atctgtatca	tcctcgatac	caacaacggt	agaaagtgtt	100
acaatatcta	ctacaaaata	tacaactagt	gactttatag	agatatttgg	150
cattgtttca	ctaattttat	tattggccgt	ggcgattttc	tgtattatat	200
tatttctgta	gtggacggtc	tcgtaaacia	gaaacaaata	tattatagat	250
tttaactcag	ataaatgtct	ggaataatta	aatctatcgt	tttgagcgga	300
ccatctgggt	ccggcaagac	agctatagtc	aggagactct	tacaagatta	350
tggaaatata	tttggaattg	tggtatccca	taccactaga	tttcctcgtc	400
ctatggaacg	agaaggtgtc	gactaccatt	acgttaacag	agaggcc	447

<210> 10

<211> 40

<212> DNA

<213> artificial sequence

<220>

<223> primer P3

<400> 10

gatacctatc acggagaaat tagatcctga tagaatcgcg 40

<210> 11

<211> 22

<212> DNA  
<213> artificial sequence

<220>  
<223> primer P1

<400> 11  
attaaacgca aatatccatg gg 22

<210> 12  
<211> 27  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer F2

<400> 12  
gcggtaccct ggggttaggc gatagag 27

<210> 13  
<211> 20  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer P5

<400> 13  
atttctccgt gataggtatc 20

<210> 14  
<211> 22  
<212> DNA  
<213> artificial sequence

<220>  
<223> primer P5

<400> 14  
ggcctctctg ttaacgtaat gg 22

<210> 15  
<211> 22  
<212> DNA  
<213> artificial sequence

<220>

<223> primer P2

<400> 15

gcgtcgaagt ttgagcatgt gc 22

<210> 16

<211> 40

<212> DNA

<213> artificial sequence

<220>

<223> primer P4

<400> 16

ctctagcgcc taaccccagg cgaccgacga caacctttat 40

<210> 17

<211> 840

<212> DNA

<213> feline infectious peritonitis virus

<220>

<223>

<400> 17

aaaccaaggc atataatccc gacgaagcat ttttggtttg aactaaacaa a 51

atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96  
Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val  
1 5 10 15

tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141  
Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys  
20 25 30

att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186  
Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly  
35 40 45

gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231  
Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val  
50 55 60

ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276  
Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln  
65 70 75

ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta	321
Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu	
80 85 90	
tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct	366
Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser	
95 100 105	
gag tac caa gtt tcc aga tat gta atg ttc ggc ttt agt gtt gca	411
Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala	
110 115 120	
ggt gca gtt gta acg ttt gca ctt tgg atg atg tat ttt gtg aga	456
Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg	
125 130 135	
tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat	501
Ser Val Gln Leu Tyr Arg Arg Thr Lys Ser Trp Trp Ser Phe Asn	
140 145 150	
cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt	546
Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser	
155 160 165	
tat gtg ctt ccc tta gat ggt act cct aca ggt gtt acc ctt act	591
Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr	
170 175 180	
cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt	636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly	
185 190 195	
ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca	681
Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr	
200 205 210	
cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa	726
Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys	
215 220 225	
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct	771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala	
230 235 240	
ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat	816
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His	
245 250 255	
gaa aaa tta tta cat atg gtg taa	840
Glu Lys Leu Leu His Met Val	
260	



<210> 18  
 <211> 1144  
 <212> DNA  
 <213> feline infectious peritonitis virus

<220>

<223>

<400> 18

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Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser	
1 5 10 15	
aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat	90
Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp	
20 25 30	
ata cct ttg tca ttc tac aac ccc att acc ctc gaa caa gga tct	135
Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser	
35 40 45	
aaa ttt tgg aat tta tgt ccg aga gac ctt gtt ccc aaa gga ata	180
Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile	
50 55 60	
ggt aat aag gat caa caa att ggt tat tgg aat aga cag att cgt	225
Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg	
65 70 75	
tat cgt att gta aaa ggc cag cgt aag gaa ctc gct gag agg tgg	270
Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp	
80 85 90	
ttc ttt tac ttc tta ggt aca gga cct cat gct gat gct aaa ttc	315
Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe	
95 100 105	
aaa gac aag att gat gga gtc ttc tgg gtt gca agg gat ggt gcc	360
Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala	
110 115 120	
atg aac aag ccc aca acg ctt ggc act cgt gga acc aat aac gaa	405
Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu	
125 130 135	
tcc aaa cca ctg aga ttt gat ggt aag ata ccg cca cag ttt cag	450
Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln	
140 145 150	
ctt gaa gtg aac cgt tct agg aac aat tca agg tct ggt tct cag	495

Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln	
				155					160					165	
tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac	540
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His	
				170					175					180	
cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc	585
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala	
				185					190					195	
gtg	ctt	gaa	aaa	tta	ggc	gtt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
				200					205					210	
aaa	cct	aga	gaa	cgt	agt	gat	tcc	aaa	cct	agg	gac	aca	aca	cct	675
Lys	Pro	Arg	Glu	Arg	Ser	Asp	Ser	Lys	Pro	Arg	Asp	Thr	Thr	Pro	
				215					220					225	
aag	aat	gcc	aac	aaa	cac	acc	tgg	aag	aaa	act	gca	ggc	aag	gga	720
Lys	Asn	Ala	Asn	Lys	His	Thr	Trp	Lys	Lys	Thr	Ala	Gly	Lys	Gly	
				230					235					240	
gat	gtg	aca	act	ttc	tat	ggc	gct	aga	agt	agt	tca	gct	aac	ttt	765
Asp	Val	Thr	Thr	Phe	Tyr	Gly	Ala	Arg	Ser	Ser	Ser	Ala	Asn	Phe	
				245					250					255	
ggc	gat	agt	gat	ctc	gtt	gcc	aat	ggc	aac	gct	gcc	aaa	tgc	tac	810
Gly	Asp	Ser	Asp	Leu	Val	Ala	Asn	Gly	Asn	Ala	Ala	Lys	Cys	Tyr	
				260					265					270	
cct	cag	ata	gct	gaa	tgt	gtt	cca	tca	gtg	tct	agc	ata	atc	ttt	855
Pro	Gln	Ile	Ala	Glu	Cys	Val	Pro	Ser	Val	Ser	Ser	Ile	Ile	Phe	
				275					280					285	
ggc	agt	caa	tgg	tct	gct	gaa	gaa	gct	ggc	gat	caa	gtg	aaa	gtc	900
Gly	Ser	Gln	Trp	Ser	Ala	Glu	Glu	Ala	Gly	Asp	Gln	Val	Lys	Val	
				290					295					300	
acg	ctc	act	cac	acc	tac	tac	ctg	cca	aag	gat	gat	gcc	aaa	act	945
Thr	Leu	Thr	His	Thr	Tyr	Tyr	Leu	Pro	Lys	Asp	Asp	Ala	Lys	Thr	
				305					310					315	
agt	caa	ttc	cta	gaa	cag	att	gac	gct	tac	aag	cga	cct	tct	gaa	990
Ser	Gln	Phe	Leu	Glu	Gln	Ile	Asp	Ala	Tyr	Lys	Atg	Pro	Ser	Glu	
				320					325					330	
gtg	gct	aag	gat	cag	agg	caa	aga	aga	tcc	cgt	tct	aag	tct	gct	1035
Val	Ala	Lys	Asp	Gln	Arg	Gln	Arg	Arg	Ser	Arg	Ser	Lys	Ser	Ala	
				335					340					345	

gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	1080
Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	
350 355 360	

aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt	1125
Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val	
365 370 375	

acg aac taa acgcatgctc	1144
Thr Asn	

<210> 19

<211> 1979

<212> DNA

<213> feline leukemia virus

<220>

<223>

<400> 19

accaccaatc aagacctctc ggacagcccc agctcagacg atccatcaag	50
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atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc	95
Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu	
1 5 10 15	

tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp	
20 25 30	

ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr	
35 40 45	

tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230
Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr	
50 55 60	

tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val	
65 70 75	

gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu	
80 85 90	

aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365
Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys	
95 100 105	

tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr	
110 115 120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys	
125 130 135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp	
140 145 150	
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser	
155 160 165	
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser	
170 175 180	
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys	
185 190 195	
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680
Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg	
200 205 210	
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725
Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser	
215 220 225	
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770
Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn	
230 235 240	
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr	
245 250 255	
ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc	860
Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala	
260 265 270	
cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg	905
Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly	
275 280 285	
acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc	950
Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala	

290										295					300					
tta	aat	gcc	acc	gac	ccc	aac	aaa	act	aaa	gac	tgt	tgg	ctc	tgc	995					
Leu	Asn	Ala	Thr	Asp	Pro	Asn	Lys	Thr	Lys	Asp	Cys	Trp	Leu	Cys						
				305					310					315						
ctg	gtt	tct	cga	cca	ccc	tat	tac	gaa	ggg	att	gca	atc	tta	ggg	1040					
Leu	Val	Ser	Arg	Pro	Pro	Tyr	Tyr	Glu	Gly	Ile	Ala	Ile	Leu	Gly						
				320					325					330						
acc	tac	agc	aac	caa	aca	aac	ccc	ccc	cca	tcc	tgc	cta	tct	act	1085					
Asn	Tyr	Ser	Asn	Gln	Thr	Asn	Pro	Pro	Pro	Ser	Cys	Leu	Ser	Ile						
				335					340					345						
ccg	caa	cac	aaa	cta	act	ata	tct	gaa	gta	tca	ggg	caa	gga	atg	1130					
Pro	Gln	His	Lys	Leu	Thr	Ile	Ser	Glu	Val	Ser	Gly	Gln	Gly	Met						
				350					355					360						
tgc	ata	ggg	act	gtt	cct	aaa	acc	cac	cag	gct	ttg	tgc	aat	aag	1175					
Cys	Ile	Gly	Thr	Val	Pro	Lys	Thr	His	Gln	Ala	Leu	Cys	Asn	Lys						
				365					370					375						
aca	caa	cag	gga	cat	aca	ggg	gcg	cac	tat	cta	gcc	gcc	ccc	aac	1220					
Thr	Gln	Gln	Gly	His	Thr	Gly	Ala	His	Tyr	Leu	Ala	Ala	Pro	Asn						
				380					385					390						
ggc	acc	tat	tgg	gcc	tgt	aac	act	gga	ctc	acc	cca	tgc	att	tcc	1265					
Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser						
				395					400					405						
atg	gcg	gtg	ctc	aat	tgg	acc	tct	gat	ttt	tgt	gtc	tta	atc	gaa	1310					
Met	Ala	Val	Leu	Asn	Trp	Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu						
				410					415					420						
tta	tgg	ccc	aga	gtg	act	tac	cat	caa	ccc	gaa	tat	gtg	tac	aca	1355					
Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr						
				425					430					435						
cat	ttt	gcc	aaa	gct	gtc	agg	ttc	cga	aga	gaa	cca	ata	tca	cta	1400					
His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Arg	Glu	Pro	Ile	Ser	Leu						
				440					445					450						
acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcc	1445					
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala						
				455					460					465						
gcg	ggg	gtc	gga	aca	ggg	act	aaa	gcc	ctc	ctt	gaa	aca	gcc	cag	1490					
Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln						
				470					475					480						
ttc	aga	caa	cta	caa	atg	gcc	atg	cac	aca	gac	atc	cag	gcc	cta	1535					

Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu		
				485					490					495		
gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580	
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser		
				500					505					510		
gaa	gta	gtc	tta	caa	aac	aga	cgg	ggc	cta	gat	att	cta	ttc	tta	1625	
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu		
				515					520					525		
caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc	1670	
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe		
				530					535					540		
tat	gcg	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta	1715	
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu		
				545					550					555		
aga	gaa	aga	cta	aaa	cag	cgg	caa	caa	ctg	ttt	gac	tcc	caa	cag	1760	
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln		
				560					565					570		
gga	tgg	ttt	gaa	gga	tgg	ttc	aac	aag	tcc	ccc	tgg	ttt	aca	acc	1805	
Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr		
				575					580					585		
cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att	1850	
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile		
				590					595					600		
ctc	ctc	ttc	ggc	cca	tgc	atc	ctt	aac	cga	tta	gta	caa	ttc	gta	1895	
Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val		
				605					610					615		
aaa	gac	aga	ata	tct	gtg	gta	cag	gct	tta	att	tta	acc	caa	cag	1940	
Lys	Asp	Arg	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln		
				620					625					630		
tac	caa	cag	ata	aag	caa	tac	gat	ccg	gac	cga	cca	tga			1979	
Tyr	Gln	Gln	Ile	Lys	Gln	Tyr	Asp	Pro	Asp	Arg	Pro					
				635					640							